

SEQUENCE LISTING

(1) GENERAL INFORMATION

(i) APPLICANT: Hermeking, Heiko  
Vogelstein, Bert  
Kinzler, Kenneth

(ii) TITLE OF THE INVENTION: 14-3-3 SIGMA ARREST THE CELL  
CYCLE

(iii) NUMBER OF SEQUENCES: 5

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Banner & Witcoff  
(B) STREET: 1001 G Street, NW  
(C) CITY: Washington  
(D) STATE: DC  
(E) COUNTRY: USA  
(F) ZIP: 20001

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette  
(B) COMPUTER: IBM Compatible  
(C) OPERATING SYSTEM: DOS  
(D) SOFTWARE: FastSEQ for Windows Version 2.0

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:  
(B) FILING DATE: 18-DEC-1997  
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER:  
(B) FILING DATE:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Kagan, Sarah A  
(B) REGISTRATION NUMBER: 32141  
(C) REFERENCE/DOCKET NUMBER: 1107.72886

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 202-508-9100  
(B) TELEFAX: 202-508-9299  
(C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1320 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GAGAGACACA	GAGTCCGGCA	TTGGTCCCAG	GCAGCAGTTA	GCCCGCCGCC	CGCCTGTGTG	60
TCCCCAGAGC	CATGGAGAGA	GCCAGTCTGA	TCCAGAAGGC	CAAGCTGGCA	GAGCAGGCCG	120
AACGCTATGA	GGACATGGCA	GCCTTCATGA	AAGGCGCCGT	GGAGAAGGGC	GAGGAGCTCT	180
CCTGCGAAGA	GCGAAACCTG	CTCTCAGTAG	CCTATAAGAA	CGTGGTGGGC	GGCCAGAGGG	240
CTGCCCTGGAG	GGTGCCTGTCC	AGTATTGAGC	AGAAAAGCAA	CGAGGAGGGC	TCGGAGGAGA	300
AGGGGCCCGA	GGTGCCTGTAG	TACCGGGAGA	AGGTGGAGAC	TGAGCTCCAG	GGCGTGTGCG	360
ACACCGTGCT	GGGCCTGCTG	GACAGCCACC	TCATCAAGGA	GGCCGGGGAC	GCCGAGAGCC	420
GGGTCTCTA	CCTGAAGATG	AAGGGTACT	ACTACCGCTA	CCTGGCCGAG	GTGGCCACCG	480
GTGACGACAA	GAAGCGCATC	ATTGACTCAG	CCCGGTCAAG	CTACCAGGAG	GCCATGGACA	540
TCAGCAAGAA	GGAGATGCCG	CCCACCAACC	CCATCCGCCT	GGGCCTGGCC	CTGAACCTTT	600
CCGTCTTCCA	CTACGAGATC	GCCAACAGCC	CCGAGGAGGC	CATCTCTCTG	GCCAAGACCA	660
CTTTCGACGA	GGCCATGGCT	GATCTGCACA	CCCTCAGCGA	GGACTCCTAC	AAAGACAGCA	720
CCCTCATCAT	GCAGCTGCTG	CGAGACAAACC	TGACACTGTG	GACGGCCGAC	AACGCCGGGG	780
AAGAGGGGGG	CGAGGCTCCC	CAGGAGCCCC	AGAGCTGAGT	TGAGCTGGCC	ACCGCCCCGC	840
CCTGCCCCCT	CCAGTCCCCC	ACCCCTGCCGA	GAGGACTAGT	ATGGGGTGGG	AGGCCACC	900
CTTCTCCCCCT	AGGCCTGTT	CTTGCTCCAA	AGGGCTCCGT	GGAGAGGGAC	TGGCAGAGCT	960
GAGGCCACCT	GGGGCTGGGG	ATCCCACCTCT	TCTTGCAGCT	GTTGAGCGCA	CCTAACCACT	1020
GGTCATGCC	CCACCCCTGC	TCTCCGCACC	CGCTTCCTCC	CGACCCCAAGG	ACCAGGCTAC	1080
TTCTCCCCCTC	CTCTTGCCTC	CCTCCTGCC	CTGCTGCCTC	TGATCGTAGG	AATTGAGGAG	1140
TGTCCCGCCT	TGTGGCTGAG	AACTGGACAG	TGGCAGGGGC	TGGAGATGGG	TGTGTGTGTG	1200
TGTGTGTGTG	TGTGTGTGTG	CGCGCGCGCC	AGTGCAAGAC	CGAGACTGAG	GGAAAGCATG	1260
TCTGCTGGGT	GTGACCATGT	TTCCCTCTAA	TAAAGTTCCC	CTGTGACACT	CAAAAAAAA	1320

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 248 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Glu	Arg	Ala	Ser	Leu	Ile	Gln	Lys	Ala	Lys	Leu	Ala	Glu	Gln	Ala
1				5				10					15		
Glu	Arg	Tyr	Glu	Asp	Met	Ala	Ala	Phe	Met	Lys	Gly	Ala	Val	Glu	Lys
				20				25					30		
Gly	Glu	Glu	Leu	Ser	Cys	Glu	Glu	Arg	Asn	Leu	Leu	Ser	Val	Ala	Tyr
				35				40					45		

Lys Asn Val Val Gly Gly Gln Arg Ala Ala Trp Arg Val Leu Ser Ser  
 50 55 60  
 Ile Glu Gln Lys Ser Asn Glu Glu Gly Ser Glu Glu Lys Gly Pro Glu  
 65 70 75 80  
 Val Arg Glu Tyr Arg Glu Lys Val Glu Thr Glu Leu Gln Gly Val Cys  
 85 90 95  
 Asp Thr Val Leu Gly Leu Leu Asp Ser His Leu Ile Lys Glu Ala Gly  
 100 105 110  
 Asp Ala Glu Ser Arg Val Phe Tyr Leu Lys Met Lys Gly Asp Tyr Tyr  
 115 120 125  
 Arg Tyr Leu Ala Glu Val Ala Thr Gly Asp Asp Lys Lys Arg Ile Ile  
 130 135 140  
 Asp Ser Ala Arg Ser Ala Tyr Gln Glu Ala Met Asp Ile Ser Lys Lys  
 145 150 155 160  
 Glu Met Pro Pro Thr Asn Pro Ile Arg Leu Gly Leu Ala Leu Asn Phe  
 165 170 175  
 Ser Val Phe His Tyr Glu Ile Ala Asn Ser Pro Glu Glu Ala Ile Ser  
 180 185 190  
 Leu Ala Lys Thr Thr Phe Asp Glu Ala Met Ala Asp Leu His Thr Leu  
 195 200 205  
 Ser Glu Asp Ser Tyr Lys Asp Ser Thr Leu Ile Met Gln Leu Leu Arg  
 210 215 220  
 Asp Asn Leu Thr Leu Trp Thr Ala Asp Asn Ala Gly Glu Glu Gly Gly  
 225 230 235 240  
 Glu Ala Pro Gln Glu Pro Gln Ser  
 245

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 7680 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GGATCCCAGC	CTGCCCCCTCC	ACTTCTCTCC	CAAGCCAGGT	CCCGGCATGG	GTGGGTTATG	60
CTCATGCTGG	CAATACTTGA	AACGGGTTTA	TTAATGCTGG	GTATTTGCA	CAATTTATA	120
GACCTCTTT	CTACATAGTC	TTTTTAAAT	GGAAGGAGAA	AATGTCAGCC	ACATTACTGT	180
CTGTGTAGTG	CCAGGTGAAG	GGTTATCAGA	AGGCTGGTTG	GTTTAATAA	GTTTATTCCA	240
AGAGACCTTC	TGGCTGGAAT	GAGTGAGAGT	GTGTGTGCAT	GTGTGTGTGT	GTTCATGTGT	300
GCCCTGTATG	AATGTGGCTG	GCTCCCAGAT	CCCCTGGGCT	GCCCCCTGCC	CCATCCCCCTT	360
TGAGTATCAG	AAGCACTCTG	AGCCAAGGGG	ACAGGGGGCA	CGTGCACGG	TCACGAGAAA	420
ACCCCTGGGCT	CCCACTGGGG	CTCAGCCCAG	CCTCCTATCT	TTCCCTCTTC	TATGGACTTC	480
AGACAGCCAG	TGTCTGGGGA	CTCTGCCACT	CTACCCCCAG	CCCTACCCAC	CAGCCCCCAG	540
GTGAGGCTTC	CAGCTGGGAC	CTGCCAGAC	AGGCTGAGCC	TGGGCGTGGT	GGGTGGGTG	600
ATGGCTCTGG	GGAGCGGCTG	CCATCCTACA	AGCCACACCC	CCTCCTCTGA	GCTCTGAATA	660
TGGGACCCAG	TGCCAGGAGC	TGGAAGACAA	GGTGTCTG	CCAAACGGGA	CCTCCATCCA	720
GAGAAAAGGA	AGAAGGTGCA	GGGTGGGCCA	AGAGGCAAGT	GAAGGTTGGC	CTGAGTCTGG	780
GCCGGAAACT	CAGAGGATGT	TTCTCCTCTG	CTGGGAGCTG	TAGTTCTTA	TCAAAATAGA	840

TATTGTTCCA	CCATCCCCCT	CCTTGGCCCT	TCAAGTGGGC	TGAAGCCTTG	GAAAGTGACA	900
TAGGAAGTCC	CCAGATCTTG	CCCTTCTCAC	TCCAGAGGGCT	AGTGGTCACA	GACAGCTGGG	960
AATGGCAGCC	ACAGAGGGTC	CCTCTGGAGA	AACAGCTTC	CCCCAGCCTC	AGGGCCCTGG	1020
GCATCACTGC	AGTGGCCCTG	GGAGGTGAGG	AAGAAGCTGG	CTAGAGGAGG	GGGCTCCAC	1080
CTACCTTTA	TTAAGCCAG	TATTCTTGT	TCTCTGTTGT	AATAAAACTT	CAGTTTATAA	1140
GAGTTGCTTT	GCTTTGGTTT	GGTTTTGTT	TGCTTTCTC	TTGCTGAGGC	CCCAACTGGG	1200
AGCCCTCTGT	TCTTTCAGAC	AAATTTGGTT	CTTCTCTGGG	GAGACTGTGA	GAAGGCAGGC	1260
AGCCCAGTGA	TCTGGCTACA	TTTCCCTCA	CCTGGCTGGA	GCTCTGTCCG	CTGGAGGAAG	1320
AGCAGAGAGG	GCTGCGGCTG	AGCCCCCATG	GGCACGTGAA	AAGAGGCCAT	CCTGTCCCCT	1380
CTTTGTCCCC	TCCACCTTCC	CCTGCCCTAG	GGGCTTGGAG	ACCCCCAATT	CTTCTTCCCT	1440
ACTGCCTTTC	CACTCCGATC	CCCAATGAGT	GCCCAGCTAA	AAAAATGTTT	GAGACAGTAG	1500
ATTCCAGTTT	GAGAGCCGGA	GCTTCCCTGG	CTACCACCTC	CAACCTGGGC	ACCAGGGCCC	1560
AGCCAGACAA	CTCATAACAC	TGGCCCACCT	CTCTGGTATC	TCCCTCAGGA	GGACACCTGT	1620
CAGGATTITG	CCATCTCTG	CACAGCCTGA	GGGGAGCTAA	CAGGCTCTT	TGCAGAGGGT	1680
TAGCTGGTAA	GACCGTTCT	TCCCTGTCGG	CCAGCACTGC	CCGCTCCCT	CCACACACCA	1740
TCTCATCTTC	ATCCATGCC	TCGCCAACCC	CATGGAGCCC	GTCCATCTGT	CTGGTGTGTG	1800
GTGCGGTGTG	TGTGCTGGT	GTGGTAGGTT	CTCCAGGGAC	TCCCCGCTAA	GCAGAAGGAT	1860
CGGGATATAG	GGCAAGGCTA	AAAGCCAGC	CCCATTTGTGG	ACTGAGGAAG	TACGTTCGCG	1920
CAGAGCAGCT	CTCCAGCTGG	AAGAGGAGGT	GGAGGGTGAG	GCTGGGGAGA	GGATGGCGAA	1980
CCTGCCCTGA	GGTGCCTGGG	TCTGTGCTGG	TGGGGCTCTG	GTATGCAGGG	GCCACCGGTC	2040
ACTAACACTC	TTATGTCTG	GCTTCTGTC	CCCGCTGAGC	TTTCTCTCAC	CCGCCCGTTT	2100
TCTCTCCTGC	TTCATTGCT	GCTGCCCTAAG	CCTTGGCCCT	TCTCTCGGGC	AGAGGCAGGT	2160
GCTGTGGCAG	CACCTCTCCC	CACCACCGGG	CCCTGCAGG	CCGCCTCCCT	CCTCCCAGGC	2220
CTGCTAACCC	TCTCTCTTCT	CCTCTTTGC	TGTCTGCGG	GGGATCTCCA	GTGTGTGCGG	2280
GGGCTTAAGG	ACCTCCTGAG	GACCGCTGCT	CTCTGCCTCT	CCAGGAATGG	CCTGGGGGGA	2340
GCCAGGCACC	CGGCACCTCC	ACCTCCCTAA	CCTGTGGCCC	ATCTGCCACC	ATCTGTGCC	2400
ACAGGGCTG	CCCCCCCAGCC	TGCCCAGCCT	GTGTGCTCTC	TAGGACCCCCA	TAGGGGGCAG	2460
GGGCTGGCCT	CTTGGCCCCA	TTCCCGCTCC	ATGCCGGCCA	GAGTGTAGAA	AGCCATAACG	2520
CACGAGCCA	TCAGCACAAT	AATGTGACTC	TACGCTGATA	TGCTCCCTCT	CTCCTCCACT	2580
GACTTCCCCT	TCCCAGATT	GTGAGGTGTC	AAGACTAGGA	ATCTGGCCTT	AGAGCCTGCC	2640
CCTCCACCCCC	CTCAGATCAG	GCATAGCCAT	AGTCAAGCCC	AGCAGGTTTC	CTCAGGAGCT	2700
GTCTGGGGTG	TTGATGGT	ATGACGCTGC	TGAACAAGTT	TGGTGA	TGTGTGTG	2760
ACTGGCTTGA	TACTGTTCCC	ACGGCCTGTC	CACCTCCCAC	CCCCAACCT	CCACCAGAGT	2820
AGGTAGGATG	TAGGGAGGGT	GCGTCCGCC	TTGCTCTAG	GCAC	TGAGGAGG	2880
CCGTGCACAG	CCCCATACAC	TTCAGGGCG	TAAGGAAAG	AGCTGAGCCA	AGGAAAATCA	2940
GCTGAGCCC	GGGCTGGGG	CTGCTTGTCT	GCTATCCTGT	ACCTTTTTT	TTTTAACCA	3000
AAATAAAGAT	TCCCCCTTTC	TTGCCATACC	ATTGGCTGTC	TGGTGGCC	TTTACTTTGG	3060
GGCCCAGGG	TGGGACCTGC	AGTGGCGT	TGAAACATAT	GGCTCCCCCT	CGCTCCCAGC	3120
TTTCTTCCAG	CTGGCCAGTG	CTGCTCTGG	GATTACAAG	CACAA	CGAGGAGG	3180
CACAGGAAA	GTGGCTGACA	TCCTTTCAC	TCTGCCCTC	CAGAACTCTT	GGTCTCAATT	3240
CCAGACACCA	CCCAGCCTA	GCTGACCTCT	GGATTCTGAT	AGGTCCCAGT	GCAGGCTGAG	3300
ACAGAGGGTT	TAACTCCAGT	TTGGGACTGC	CATACCCATG	AACTGAGCCC	AGCCCAGGGT	3360
AACGATCTCA	TGGAAAAC	TCTCTCCCCA	GTGCTGAC	TACATCAAGA	TACACACATG	3420
TGCATACACT	GTACTATGG	CTAAAAAAAT	ACGTACCGCT	ACCGTTTCAGC	AAGGGCTTGC	3480
CGAGTCCCCG	GCCCATTTC	TCATCTAAC	CTGTGAGGAG	GATGATGTCA	GCCTTTTAC	3540
AGATGAGGGA	ACTGAGACTC	AAGGAAGAAA	CAGGAGCTGC	CCAAGGT	CCAGCTGGCA	3600
AAGCAGCAA	TCCCAGATCG	GAACCTGATC	TCTGCCCTGA	GCTCTGAGCC	ATCTGCACTA	3660
CCCAAGGAAT	GAATACAGCG	GTGGGAGGAT	GAGATCTTGG	AGAAACCC	CTAATAGAGA	3720
ATGTATAGC	CAGTAGAGGG	CTTAGAGTT	ATCTGGGCCA	GCCTCCTTGT	TTTACTGATG	3780
GAGAAATTGA	AGCCCAGAGG	CAGGAAGGG	CCTGCCAAG	GCCTTATAAC	AGAGCTGGGA	3840
TGCAGTCCC	CACTCTGACC	TCATTCCATT	CTCTCTCCAT	AAATTCTGCA	CTGTCTCTAG	3900
ACTGGACTGG	TTTAGATGTG	GGATACTCTA	AACAGCAGTG	CCTTCAGAG	AAAAAGAAC	3960

AGAACTACGA	ATCACTTAAA	AGTAATGTAA	GCTACTCTGG	GCACACTGCC	TATGGGGTCG	4020
CCCTGCTCCA	CAAGGAGCCA	CAAAAATAAT	TAAAATAATT	TAATATCCCT	TCCCAAAGGT	4080
AACCAGTAAA	GTAAGCTCTT	GGCTAGGTAA	CTGGACTCTT	GTTCACAAC	AGCCAGTGGG	4140
AAAAGGTGCT	AGAGCTTCCT	CTGGCCACCT	GTAAATTG	ATCATTCCAA	GACAGAAACA	4200
TTTCTTAGGA	AGTCTTTCT	AGAATCTACC	TGGTGTCCCT	CCCACGTGCA	TCAGAGCCCT	4260
GTCCTCTGTC	CTCAGTGGAG	GTAGAGAGCA	AATGGTTGCT	GCTTCTTCA	TCACAACCC	4320
TCAAAGCCTA	TTATTACCA	CTAAGAAGGA	TTGGTTGACT	ATGGGCCAGA	CCCCCTGAGC	4380
CTGCTGGTAG	AATGGATGCT	GTACAGGAGG	GTGGGGAGGT	AGCAGGCAGA	ATGAGGAAAG	4440
CCCCTTGAG	CTGCAACCCC	AGCTCTGTC	CTGCTGACTC	AGACAGCTGA	CTGTGGAGCT	4500
CCATGCCCTG	CCAGGGCCTG	CTGCCTCTG	CCCGTCTGAG	CTCCTGAACT	TGGGAAATGG	4560
AGGCCAGAG	GCAAAGGGAG	GTACCTGAGA	CAGGAACGTG	GTCAGGATCA	ACAGGCCAGA	4620
GCGGGCAGGA	GGTATCAGGC	AGCCTGGCTC	CCAGATGCAC	CCCTGAGCTC	CAGCAGGGGA	4680
GGAGTAGGAA	TGAAGGGGCT	TCCTTGCCT	TGCTCATGGC	TATGCGGAGG	CGGTGAACCA	4740
CCACCAAGGTC	CTCTGGCTTA	AGTGGCGGA	ACCAAATGGT	CCCTCCCTGG	ACTCAGGCTC	4800
CAAAGTTCT	GGGCTGCCT	TCCAGGTCC	CAGTGTCTG	GGATCTCCAG	CTTCCCCAG	4860
GACTTGGGA	AGCCCCGGCT	GGATGACTAG	TACAAATGAA	GGCCCTGAG	GTTCAGGAC	4920
CTGCTGAGGT	CACAGGAATA	TCCTAGATCA	AGCTTGTCCA	ACCCACGGCC	CACAGGCTGC	4980
ATGTGGCCA	GAATGGCTTT	GAATGCAGCC	CAACACAAAT	TAGTAAACTT	TCTTAAACA	5040
TTATGAGATT	TTTTTGCAA	TTTTTTTTT	TTTTTTAGCT	CATCACTTAT	TGGTAGTGTT	5100
GGTATATTTT	ATGTGTGGCC	CAAGACAATT	CTTCCAATGT	GGCCCAAGGGA	AGCCAAAAGA	5160
TTGGACACGC	CTGTCTAGA	TGGAGAGGAA	GGAGGCAGTG	CTGAGCACAT	CTGGCCATTC	5220
ATCCATCTGG	AGAGAGAAGG	CTATGGCAA	ACTGCTTCCT	CTCCCCGTGA	GACACCCAGC	5280
TGGGAAGGTC	TGGCCTTGG	TAAGTCTGG	CTTGGGGTCC	TTCTCTATT	CACAGAACCT	5340
AACTCTATGT	TAGTGTCTTG	TGAGTATATG	TTGATCATAA	AAAGTTGAC	GGGATTTTT	5400
CACATGATAA	TAATAGTTGT	CATCTGCCG	GGCATGGTGG	CTTATGCCTA	TAATTCAGC	5460
ACTTTGGAAG	GCTGAGGCAG	GTGGATCACT	TGAGGTCAAGC	TGTTCGAGAC	CAGCCTGGCC	5520
AACATGGTGA	AACCACATCT	CTACTTAAAA	AAAAAAAATT	TACAAAATT	AGCTGGGTGT	5580
GGTGGTGCAC	CCTTGTAAATC	CCAGCTACTC	GGGAGGCTGA	GGCAGGAGAA	TCACTTGAAC	5640
CCAGGAGGTG	GAGGTTGCAG	TGAGCTGAGA	TTGTGCCACT	ACACTCCAGC	CTGGGTGACA	5700
AGAGCGAAAC	TCCGTCTCAA	AAAAAAAGAA	AAAATAATA	ATAATAGTTG	CCATCCATT	5760
TACTGTGCTT	TCCATTAACT	CGTGTAAATCC	TCACAAGTCC	CATTTTATAG	TTACAGGAAC	5820
TGAGGCTCAC	AGAGCTAAA	TCACTTGGCC	AAAGGCCACAA	ACAGCTATAA	GAATTACATT	5880
TAGGCAGTCT	GATTCCAAAG	ATACTAGTCT	ATTCTGTATC	TCATAGACAA	ACAATACATA	5940
TTCACTTTTT	TGTTGTTGTT	TTGTTTGAG	ACGGAGTCTT	GCTCTGTAC	CCAGGCTGG	6000
GTGCAGTGGC	GCCATCTCGG	CTCACTGCAA	CGTCCGCCTC	CCGGGTTCAA	GGGATTCTCC	6060
TGCCTCAGCC	TCCCCAGTAG	CTGGGACTAC	AGGCATGTGC	CACCATGCC	GGCTAATT	6120
TTGTATTTT	AGTAGAGACA	GGGTTTCCCT	GGGTTAGCCA	GAATGGTCTC	GATCTCTGA	6180
CCTTGTGATC	CACCCACCTC	AGCCTCCAA	AGTGCTGAGA	TGACAGGC	GAGCCACCGC	6240
GTCCGACCTA	TATTCACTAT	TTATAAATTG	GAGAGAATAA	AAAATCAA	AGGGCCAGGT	6300
GTAGTGACTC	ACACCTGTAA	TCCCAGCACT	TTGGGAAGCC	AAGGCAGGAG	GATTGCTTGA	6360
ACCCAGAAGT	TCGAGACCGAG	CCTGGCAAC	ATGGTGCAGAC	CCTGCTCTA	AAAAAAATAC	6420
AAAAATTAGC	TGGCGTTGT	GGTGAGCACC	TTATTCTTAG	GAAGCTGAGG	CAGGAGGATC	6480
ACCTGAGGCC	AAGGAGGTG	AGACTGCAGT	GAGCTGTGAT	CATACCACTG	TACTTCAGCC	6540
TGGACATCAG	AGTAAGACCC	TATCTCTAAA	AAGGAAATTG	AGAAGAAAGA	AAATCAAAGG	6600
GAAGCAAAAT	CACTCACTCT	CACTACCTCA	AGATAACCC	TAGAAGTTGG	TATTTTAGTG	6660
TGGTTCCCTAT	TGTTTTCTGT	GTCAGTCTC	TGATTTGAGC	AAAATCTTTG	GGACGTCAA	6720
CTTAAAATCC	CCTTTACTTC	CTTGGAAACC	CTGTAGCATT	AGCCCAGACA	TGTCCCTACT	6780
CCTCCTTGTG	GCAAAGAGAA	GGATCTCGTC	TTTGGTCCCC	AGAGTCTG	CCTAACGCC	6840
CCTCCAGGAG	GGAAAGATGAG	TGTTCAAGACA	CTCAGAGTAG	CTGGGGGAGA	CACAGGCC	6900
TGAAATTATC	CTGGCTAAC	TATTAGGTG	GCAGAATCCC	AGTGAAGGGA	GCCCTACCTC	6960
TGAGCCCCAT	CTAAGCTTTG	GCTATGGGTG	GGCAGATAA	GCAGGAATCC	ATCCCTATAG	7020
GCTCAATGCC	AACACCCCTTA	GGTGAACACTC	TTGATGAAAC	TTGAGGCCAG	GGCTCCGGCA	7080

AGCAGGGAAA	GAACGTTGGC	AACAGAGGTC	TCCATCTCTG	AGGACTCTGC	CAGGGGTCAG	7140
AGATGGGCA	ATGGTCAAAA	GGAAAGGAACA	GGCCAGGCAC	AGTGGCTCAT	GCCCATAATC	7200
CCAGCACTT	GGGAGGCTGA	GGCAGGAGGA	TCGCTTGAGC	CCAGGAGTTT	GAGACCTGCC	7260
TGGGCAATGT	AGTGAGATCT	GCTCTCTATT	AAAAAAAAAA	AAAAGGAAA	GAACAAGTAA	7320
ACTTCTGAGA	AACAGGCTGG	GGGAGGCATC	ACGTAGCTGG	AATTGCTGCC	CCATAAAACA	7380
GAATGGTATG	TGTCACTGCC	ACCTCCCTT	CTCAGTCCTC	TCTCTCCCCA	GGTTGCTAGC	7440
GTCCCCCTGG	GGGATCAAAC	TGGACTGCTT	CCCAGCCTCA	GACAGAGAGC	AGTCTGAGTC	7500
AGGCAGGAAA	GTGGGACAGC	CGGGGAGCTG	GACCCCACCC	TCTGTGAGCC	CCGCTGGTAC	7560
CTGATGGCAT	GTGGCTTGGA	GAGGGCAGGT	GACCTGGCGT	GGAGGGCCAG	AGGGTAAATC	7620
CTCAAACAAG	TGGCAACAGG	CCACCAACTT	GAAAGGAAA	ATTGTGTAGT	GATGGGAAAT	7680

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

AGGCATGTGC CACCATGCC 20

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GTAGCATTAG CCCAGACATG TCC 23